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SEQUENCE LISTING

GENERAL INFORMATION:

- T340X
- AM
- (i) APPLICANT: Amara, Susan G
Arriza, Jeffrey L
 - (ii) TITLE OF INVENTION: Amino Acid Transporters and Uses
 - (iii) NUMBER OF SEQUENCES: 17
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Allegretti & Witcoff, Ltd.
 - (B) STREET: 10 South Wacker Drive, Suite 3000
 - (C) CITY: Chicago
 - (D) STATE: IL
 - (E) COUNTRY: USA
 - (F) ZIP: 60606
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/140,729
 - (B) FILING DATE: 20 OCT 1993
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Noonan, Kevin E
 - (B) REGISTRATION NUMBER: 35,303
 - (C) REFERENCE/DOCKET NUMBER: 93,509
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312-715-1000
 - (B) TELEFAX: 312-715-1234
 - (C) TELEX: 910-221-5317

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGRGCRATG AARATGGCAG CCAGGGCYTC ATACAGGGCT GTGCCRTCCA TGTRATGGT 60
RGC 63

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..30

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 31..1626

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1626..1680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACCTCTAGC TCGGAGCGGC GTGTAGCGCC ATG GAG AAG AGC AAC GAG ACC AAC 54
Met Glu Lys Ser Asn Glu Thr Asn
1 5

GGC TAC CTT GAC AGC GCT CAG GCG GGG CCT GCG GCC GGG CCC GGA GCT 102
Gly Tyr Leu Asp Ser Ala Gln Ala Gly Pro Ala Ala Gly Pro Gly Ala
10 15 20

CCG GGG ACC GCG GCG GGA CGC GCA CGG CGT TGC GCG CGC TTC CTG CGG 150
Pro Gly Thr Ala Ala Gly Arg Ala Arg Arg Cys Ala Arg Phe Leu Arg
25 30 35 40

CGC CAA GCG CTG GTG CTG CTC ACC GTG TCC GGG GTG CTG GCG GGC GCG 198
Arg Gln Ala Leu Val Leu Leu Thr Val Ser Gly Val Leu Ala Gly Ala
45 50 55

GGC CTG GGC GCG GCG TTG CGC GGG CTC AGC CTG AGC CGC ACG CAG GTC 246
Gly Leu Gly Ala Ala Leu Arg Gly Leu Ser Leu Ser Arg Thr Gln Val
60 65 70

35
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ACC TAC CTG GCC TTC CCC GGC GAG ATG CTG CTC CGC ATG CTG CGC ATG	294
Thr Tyr Leu Ala Phe Pro Gly Glu Met Leu Leu Arg Met Leu Arg Met	
75 80 85	
ATC ATC CTG CCG CTG GTG GTC TGC AGC CTG GTG TCG GGC GCC GCC TCG	342
Ile Ile Leu Pro Leu Val Val Cys Ser Leu Val Ser Gly Ala Ala Ser	
90 95 100	
CTC GAT GCC AGC TGC CTC GGG CGT CTG GGC GGC ATC CGT GTC GCC TAC	390
Leu Asp Ala Ser Cys Leu Gly Arg Leu Gly Gly Ile Arg Val Ala Tyr	
105 110 115 120	
TTT GGC CTC ACC ACA CTG AGT GCC TCG GCG CTC GCC GTG GCC TTG GCG	438
Phe Gly Leu Thr Thr Leu Ser Ala Ser Ala Leu Ala Val Ala Leu Ala	
125 130 135	
TTC ATC ATC AAG CCA GGA TCC GGT GCG CAG ACC CTT CAG TCC AGC GAC	486
Phe Ile Ile Lys Pro Gly Ser Gly Ala Gln Thr Leu Gln Ser Ser Asp	
140 145 150	
CTG GGG CTG GAG GAC TCG GGG CCT CCT CCT GTC CCC AAA GAG ACG GTG	534
Leu Gly Leu Glu Asp Ser Gly Pro Pro Pro Val Pro Lys Glu Thr Val	
155 160 165	
GAC TCT TTC CTC GAC CTG GCC AGA AAC CTG TTT CCC TCC AAT CTT GTG	582
Asp Ser Phe Leu Asp Leu Ala Arg Asn Leu Phe Pro Ser Asn Leu Val	
170 175 180	
GTT GCA GCT TTC CGT ACG TAT GCA ACC GAT TAT AAA GTC GTG ACC CAG	630
Val Ala Ala Phe Arg Thr Tyr Ala Thr Asp Tyr Lys Val Val Thr Gln	
185 190 195 200	
AAC AGC AGC TCT GGA AAT GTA ACC CAT GAA AAG ATC CCC ATA GGC ACT	678
Asn Ser Ser Ser Gly Asn Val Thr His Glu Lys Ile Pro Ile Gly Thr	
205 210 215	
GAG ATA GAA GGG ATG AAC ATT TTA GGA TTG GTC CTG TTT GCT CTG GTG	726
Glu Ile Glu Gly Met Asn Ile Leu Gly Leu Val Leu Phe Ala Leu Val	
220 225 230	
TTA GGA GTG GCC TTA AAG AAA CTA GGC TCC GAA GGA GAA GAC CTC ATC	774
Leu Gly Val Ala Leu Lys Lys Leu Gly Ser Glu Gly Glu Asp Leu Ile	
235 240 245	
CGT TTC TTC AAT TCC CTC AAC GAG GCG ACG ATG GTG CTG GTG TCC TGG	822
Arg Phe Phe Asn Ser Leu Asn Glu Ala Thr Met Val Leu Val Ser Trp	
250 255 260	
ATT ATG TGG TAC GTA CCT GTG GGC ATC ATG TTC CTT GTT GGA AGC AAG	870
Ile Met Trp Tyr Val Pro Val Gly Ile Met Phe Leu Val Gly Ser Lys	
265 270 275 280	

36

ATC GTG GAA ATG AAA GAC ATC ATC GTG CTG GTG ACC AGC CTG GGG AAA	918
Ile Val Glu Met Lys Asp Ile Ile Val Leu Val Thr Ser Leu Gly Lys	
285 290 295	
TAC ATC TTC GCA TCT ATA TTG GGC CAT GTT ATT CAT GGA GGA ATT GTT	966
Tyr Ile Phe Ala Ser Ile Leu Gly His Val Ile His Gly Gly Ile Val	
300 305 310	
CTG CCA CTT ATT TAT TTT GTT TTC ACA CGA AAA AAC CCA TTC AGA TTC	1014
Leu Pro Leu Ile Tyr Phe Val Phe Thr Arg Lys Asn Pro Phe Arg Phe	
315 320 325	
CTC CTG GGC CTC CTC GCC CCA TTT GCG ACA GCA TTT GCT ACC TGC TCC	1062
Leu Leu Gly Leu Leu Ala Pro Phe Ala Thr Ala Phe Ala Thr Cys Ser	
330 335 340	
AGC TCA GCG ACC CTT CCC TCT ATG ATG AAG TGC ATT GAA GAG AAC AAT	1110
Ser Ser Ala Thr Leu Pro Ser Met Met Lys Cys Ile Glu Glu Asn Asn	
345 350 355 360	
GGT GTG GAC AAG AGG ATC AGC AGG TTT ATT CTC CCC ATC GGG GCC ACC	1158
Gly Val Asp Lys Arg Ile Ser Arg Phe Ile Leu Pro Ile Gly Ala Thr	
365 370 375	
GTG AAC ATG GAC GGA GCA GCC ATC TTC CAG TGT GTG GCC GCG GTG TTC	1206
Val Asn Met Asp Gly Ala Ala Ile Phe Gln Cys Val Ala Ala Val Phe	
380 385 390	
ATT GCG CAA CTC AAC AAC ATA GAG CTC AAC GCA GGA CAG ATT TTC ACC	1254
Ile Ala Gln Leu Asn Asn Ile Glu Leu Asn Ala Gly Gln Ile Phe Thr	
395 400 405	
ATT CTA GTG ACT GCC ACA GCG TCC AGT GTT GGA GCA GCA GGC GTG CCA	1302
Ile Leu Val Thr Ala Thr Ala Ser Ser Val Gly Ala Ala Gly Val Pro	
410 415 420	
GCT GGA GGG GTC CTC ACC ATT GCC ATT ATC CTG GAG GCC ATT GGG CTG	1350
Ala Gly Gly Val Leu Thr Ile Ala Ile Ile Leu Glu Ala Ile Gly Leu	
425 430 435 440	
CCT ACT CAT GAC CTG CCT CTG ATC CTG GCT GTG GAC TGG ATT GTG GAC	1398
Pro Thr His Asp Leu Pro Leu Ile Leu Ala Val Asp Trp Ile Val Asp	
445 450 455	
CGG ACC ACC ACG GTG GTG AAT GTG GAG GGG GAT GCC CTG GGT GCA GGC	1446
Arg Thr Thr Thr Val Val Asn Val Glu Gly Asp Ala Leu Gly Ala Gly	
460 465 470	
ATT CTC CAC CAC CTG AAT CAG AAG GCA ACA AAG AAA GGC GAG CAG GAA	1494
Ile Leu His His Leu Asn Gln Lys Ala Thr Lys Lys Gly Glu Gln Glu	
475 480 485	

CTT	GCT	GAG	GTG	AAA	GTG	GAA	GCC	ATC	CCC	AAC	TGC	AAG	TCT	GAG	GAG	1542				
Leu	Ala	Glu	Val	Lys	Val	Glu	Ala	Ile	Pro	Asn	Cys	Lys	Ser	Glu	Glu					
490				495				500												
GAG	ACA	TCG	CCC	CTG	GTG	ACA	CAC	CAG	AAC	CCC	GCT	GGC	CCC	GTG	GCC	1590				
Glu	Thr	Ser	Pro	Leu	Val	Thr	His	Gln	Asn	Pro	Ala	Gly	Pro	Val	Ala					
505				510				515				520								
AGT	GCC	CCA	GAA	CTG	GAA	TCC	AAG	GAG	TCG	GTT	CTG	TGATGGGGCT				1636				
Ser	Ala	Pro	Glu	Leu	Glu	Ser	Lys	Glu	Ser	Val	Leu									
525				530																
GGGCTTTGGG												CTTGCCCTGCC		AGCAGTGATG		TCCCACCCTG		TTCA		1680

(2) INFORMATION FOR SEQ ID NO:3:

(i) **SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 532 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met 1	Glu	Lys	Ser	Asn 5	Glu	Thr	Asn	Gly	Tyr 10	Leu	Asp	Ser	Ala	Gln 15	Ala
Gly	Pro	Ala	Ala 20	Gly	Pro	Gly	Ala	Pro 25	Gly	Thr	Ala	Ala	Gly 30	Arg	Ala
Arg	Arg	Cys 35	Ala	Arg	Phe	Leu	Arg 40	Arg	Gln	Ala	Leu	Val 45	Leu	Leu	Thr
Val	Ser 50	Gly	Val	Leu	Ala	Gly 55	Ala	Gly	Leu	Gly	Ala 60	Ala	Leu	Arg	Gly
Leu 65	Ser	Leu	Ser	Arg 70	Thr	Gln	Val	Thr	Tyr	Leu 75	Ala	Phe	Pro	Gly	Glu 80
Met	Leu	Leu	Arg	Met 85	Leu	Arg	Met	Ile	Ile 90	Leu	Pro	Leu	Val	Val 95	Cys
Ser	Leu	Val	Ser 100	Gly	Ala	Ala	Ser	Leu 105	Asp	Ala	Ser	Cys	Leu 110	Gly	Arg
Leu	Gly 115	Gly	Ile	Arg	Val	Ala	Tyr 120	Phe	Gly	Leu	Thr	Thr 125	Leu	Ser	Ala
Ser 130	Ala	Leu	Ala	Val	Ala	Leu	Ala 135	Phe	Ile	Ile	Lys 140	Pro	Gly	Ser	Gly

Ala Gln Thr Leu Gln Ser Ser Asp Leu Gly Leu Glu Asp Ser Gly Pro
 145 150 155 160
 Pro Pro Val Pro Lys Glu Thr Val Asp Ser Phe Leu Asp Leu Ala Arg
 165 170 175
 Asn Leu Phe Pro Ser Asn Leu Val Val Ala Ala Phe Arg Thr Tyr Ala
 180 185 190
 Thr Asp Tyr Lys Val Val Thr Gln Asn Ser Ser Ser Gly Asn Val Thr
 195 200 205
 His Glu Lys Ile Pro Ile Gly Thr Glu Ile Glu Gly Met Asn Ile Leu
 210 215 220
 Gly Leu Val Leu Phe Ala Leu Val Leu Gly Val Ala Leu Lys Lys Leu
 225 230 235 240
 Gly Ser Glu Gly Glu Asp Leu Ile Arg Phe Phe Asn Ser Leu Asn Glu
 245 250 255
 Ala Thr Met Val Leu Val Ser Trp Ile Met Trp Tyr Val Pro Val Gly
 260 265 270
 Ile Met Phe Leu Val Gly Ser Lys Ile Val Glu Met Lys Asp Ile Ile
 275 280 285
 Val Leu Val Thr Ser Leu Gly Lys Tyr Ile Phe Ala Ser Ile Leu Gly
 290 295 300
 His Val Ile His Gly Gly Ile Val Leu Pro Leu Ile Tyr Phe Val Phe
 305 310 315 320
 Thr Arg Lys Asn Pro Phe Arg Phe Leu Leu Gly Leu Leu Ala Pro Phe
 325 330 335
 Ala Thr Ala Phe Ala Thr Cys Ser Ser Ser Ala Thr Leu Pro Ser Met
 340 345 350
 Met Lys Cys Ile Glu Glu Asn Asn Gly Val Asp Lys Arg Ile Ser Arg
 355 360 365
 Phe Ile Leu Pro Ile Gly Ala Thr Val Asn Met Asp Gly Ala Ala Ile
 370 375 380
 Phe Gln Cys Val Ala Ala Val Phe Ile Ala Gln Leu Asn Asn Ile Glu
 385 390 395 400
 Leu Asn Ala Gly Gln Ile Phe Thr Ile Leu Val Thr Ala Thr Ala Ser
 405 410 415

39
-40-

Ser Val Gly Ala Ala Gly Val Pro Ala Gly Gly Val Leu Thr Ile Ala
420 425 430

Ile Ile Leu Glu Ala Ile Gly Leu Pro Thr His Asp Leu Pro Leu Ile
435 440 445

Leu Ala Val Asp Trp Ile Val Asp Arg Thr Thr Thr Val Val Asn Val
450 455 460

Glu Gly Asp Ala Leu Gly Ala Gly Ile Leu His His Leu Asn Gln Lys
465 470 475 480

Ala Thr Lys Lys Gly Glu Gln Glu Leu Ala Glu Val Lys Val Glu Ala
485 490 495

Ile Pro Asn Cys Lys Ser Glu Glu Glu Thr Ser Pro Leu Val Thr His
500 505 510

Gln Asn Pro Ala Gly Pro Val Ala Ser Ala Pro Glu Leu Glu Ser Lys
515 520 525

Glu Ser Val Leu
530

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..30

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 31..1656

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1657..1680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAAGAAGAGA CCCTCCTAGA AAAGTAAAT ATG ACT AAA AGC AAT GGA GAA GAG
Met Thr Lys Ser Asn Gly Glu Glu
1 5

54

40

CCC	AAG	ATG	GGG	GGC	AGG	ATG	GAG	AGA	TTC	CAG	CAG	GGA	GTC	CGT	AAA	102
Pro	Lys	Met	Gly	Gly	Arg	Met	Glu	Arg	Phe	Gln	Gln	Gly	Val	Arg	Lys	
	10					15						20				
CGC	ACA	CTT	TTG	GCC	AAG	AAG	AAA	GTG	CAG	AAC	ATT	ACA	AAG	GAG	GTT	150
Arg	Thr	Leu	Leu	Ala	Lys	Lys	Lys	Val	Gln	Asn	Ile	Thr	Lys	Glu	Val	
	25				30				35						40	
GTT	AAA	AGT	TAC	CTG	TTT	CGG	AAT	GCT	TTT	GTG	CTG	CTC	ACA	GTC	ACC	198
Val	Lys	Ser	Tyr	Leu	Phe	Arg	Asn	Ala	Phe	Val	Leu	Leu	Thr	Val	Thr	
				45				50						55		
GCT	GTC	ATT	GTG	GGT	ACA	ATC	CTT	GGA	TTT	ACC	CTC	CGA	CCA	TAC	AGA	246
Ala	Val	Ile	Val	Gly	Thr	Ile	Leu	Gly	Phe	Thr	Leu	Arg	Pro	Tyr	Arg	
			60				65					70				
ATG	AGC	TAC	CGG	GAA	GTC	AAG	TAC	TTC	TCC	TTT	CCT	GGG	GAA	CTT	CTG	294
Met	Ser	Tyr	Arg	Glu	Val	Lys	Tyr	Phe	Ser	Phe	Pro	Gly	Glu	Leu	Leu	
		75					80					85				
ATG	AGG	ATG	TTA	CAG	ATG	CTG	GTC	TTA	CCA	CTT	ATC	ATC	TCC	AGT	CTT	342
Met	Arg	Met	Leu	Gln	Met	Leu	Val	Leu	Pro	Leu	Ile	Ile	Ser	Ser	Leu	
	90					95					100					
GTC	ACA	GGA	ATG	GCG	GCG	CTA	GAT	AGT	AAG	GCA	TCA	GGG	AAG	TGG	GAA	390
Val	Thr	Gly	Met	Ala	Ala	Leu	Asp	Ser	Lys	Ala	Ser	Gly	Lys	Trp	Glu	
	105				110					115					120	
TGC	GGA	GCT	GTA	GTC	TAT	TAT	ATG	ACT	ACC	ACC	ATC	ATT	GCT	GTG	GTG	438
Cys	Gly	Ala	Val	Val	Tyr	Tyr	Met	Thr	Thr	Thr	Ile	Ile	Ala	Val	Val	
				125				130						135		
ATT	GGC	ATA	ATC	ATT	GTC	ATC	ATC	ATC	CAT	CCT	GGG	AAG	GGC	ACA	AAG	486
Ile	Gly	Ile	Ile	Ile	Val	Ile	Ile	Ile	His	Pro	Gly	Lys	Gly	Thr	Lys	
			140					145					150			
GAA	AAC	ATG	CAC	AGA	GAA	GGC	AAA	ATT	GTA	CGA	GTG	ACA	GCT	GCA	GAT	534
Glu	Asn	Met	His	Arg	Glu	Gly	Lys	Ile	Val	Arg	Val	Thr	Ala	Ala	Asp	
		155					160					165				
GCC	TTC	CTG	GAC	TTG	ATC	AGG	AAC	ATG	TTA	AAT	CCA	AAT	CTG	GTA	GAA	582
Ala	Phe	Leu	Asp	Leu	Ile	Arg	Asn	Met	Leu	Asn	Pro	Asn	Leu	Val	Glu	
	170					175					180					
GCC	TGC	TTT	AAA	CAG	TTT	AAA	ACC	AAC	TAT	GAG	AAG	AGA	AGC	TTT	AAA	630
Ala	Cys	Phe	Lys	Gln	Phe	Lys	Thr	Asn	Tyr	Glu	Lys	Arg	Ser	Phe	Lys	
	185				190					195				200		
GTG	CCC	ATC	CAG	GCC	AAC	GAA	ACG	CTT	GTG	GGT	GCT	GTG	ATA	AAC	AAT	678
Val	Pro	Ile	Gln	Ala	Asn	Glu	Thr	Leu	Val	Gly	Ala	Val	Ile	Asn	Asn	
				205					210					215		

GTG TCT GAG GCC ATG GAG ACT CTT ACC CGA ATC ACA GAG GAG CTG GTC Val Ser Glu Ala Met Glu Thr Leu Thr Arg Ile Thr Glu Glu Leu Val 220 225 230	726
CCA GTT CCA GGA TCT GTG AAT GGA GTC AAT GCC CTG GGT CTA GTT GTC Pro Val Pro Gly Ser Val Asn Gly Val Asn Ala Leu Gly Leu Val Val 235 240 245	774
TTC TCC ATG TGC TTC GGT TTT GTG ATT GGA AAC ATG AAG GAA CAG GGG Phe Ser Met Cys Phe Gly Phe Val Ile Gly Asn Met Lys Glu Gln Gly 250 255 260	822
CAG GCC CTG AGA GAG TTC TTT GAT TCT CTT AAC GAA GCC ATC ATG AGA Gln Ala Leu Arg Glu Phe Phe Asp Ser Leu Asn Glu Ala Ile Met Arg 265 270 275 280	870
CTG GTA GCA GTA ATA ATG TGG TAT GCC CCC GTG GGT ATT CTC TTC CTG Leu Val Ala Val Ile Met Trp Tyr Ala Pro Val Gly Ile Leu Phe Leu 285 290 295	918
ATT GCT GGG AAG ATT GTG GAG ATG GAA GAC ATG GGT GTG ATT GGG GGG Ile Ala Gly Lys Ile Val Glu Met Glu Asp Met Gly Val Ile Gly Gly 300 305 310	966
CAG CTT GCC ATG TAC ACC GTG ACT GTC ATT GTT GGC TTA CTC ATT CAC Gln Leu Ala Met Tyr Thr Val Thr Val Ile Val Gly Leu Leu Ile His 315 320 325	1014
GCA GTC ATC GTC TTG CCA CTC CTC TAC TTC TTG GTA ACA CGG AAA AAC Ala Val Ile Val Leu Pro Leu Leu Tyr Phe Leu Val Thr Arg Lys Asn 330 335 340	1062
CCT TGG GTT TTT ATT GGA GGG TTG CTG CAA GCA CTC ATC ACC GCT CTG Pro Trp Val Phe Ile Gly Gly Leu Leu Gln Ala Leu Ile Thr Ala Leu 345 350 355 360	1110
GGG ACC TCT TCA AGT TCT GCC ACC CTA CCC ATC ACC TTC AAG TGC CTG Gly Thr Ser Ser Ser Ser Ala Thr Leu Pro Ile Thr Phe Lys Cys Leu 365 370 375	1158
GAA GAG AAC AAT GGC GTG GAC AAG CGC GTC ACC AGA TTC GTG CTC CCC Glu Glu Asn Asn Gly Val Asp Lys Arg Val Thr Arg Phe Val Leu Pro 380 385 390	1206
GTA GGA GCC ACC ATT AAC ATG GAT GGG ACT GCC CTC TAT GAG GCT TTG Val Gly Ala Thr Ile Asn Met Asp Gly Thr Ala Leu Tyr Glu Ala Leu 395 400 405	1254
GCT GCC ATT TTC ATT GCT CAA GTT AAC AAC TTT GAA CTG AAC TTC GGA Ala Ala Ile Phe Ile Ala Gln Val Asn Asn Phe Glu Leu Asn Phe Gly 410 415 420	1302

CAA Gln 425	ATT Ile	ATT Ile	ACA Thr	ATC Ile	AGC Ser 430	ATC Ile	ACA Thr	GCC Ala	ACA Thr	GCT Ala 435	GCC Ala	AGT Ser	ATT Ile	GGG Gly	GCA Ala 440	1350
GCT Ala	GGA Gly	ATT Ile	CCT Pro	CAG Gln 445	GCG Ala	GGC Gly	CTG Leu	GTC Val	ACT Thr 450	ATG Met	GTC Val	ATT Ile	GTG Val	CTG Leu 455	ACA Thr	1398
TCT Ser	GTC Val	GGC Gly	CTG Leu 460	CCC Pro	ACT Thr	GAC Asp	GAC Asp	ATC Ile 465	ACG Thr	CTC Leu	ATC Ile	ATC Ile	GCG Ala 470	GTG Val	GAC Asp	1446
TGG Trp	TTC Phe	TTG Leu 475	GAT Asp	CGC Arg	CTC Leu	CGG Arg	ACC Thr 480	ACC Thr	ACC Thr	AAC Asn	GTA Val	CTG Leu 485	GGA Gly	GAC Asp	TCC Ser	1494
CTG Leu 490	GGA Gly	GCT Ala	GGG Gly	ATT Ile	GTG Val 495	GAG Glu	CAC His	TTG Leu	TCA Ser	CGA Arg	CAT His 500	GAA Glu	CTG Leu	AAG Lys	AAC Asn	1542
AGA Arg 505	GAT Asp	GTT Val	GAA Glu	ATG Met 510	GGT Gly	AAC Asn	TCA Ser	GTG Val	ATT Ile	GAA Glu 515	GAG Glu	AAT Asn	GAA Glu	ATG Met 520	AAG Lys	1590
AAA Lys	CCA Pro	TAT Tyr	CAA Gln 525	CTG Leu	ATT Ile	GCA Ala	CAG Gln	GAC Asp	AAT Asn 530	GAA Glu	ACT Thr	GAG Glu	AAA Lys	CCC Pro 535	ATC Ile	1638
GAC Asp	AGT Ser	GAA Glu	ACC Thr 540	AAG Lys	ATG Met	TAGACTAACA TAAAGAAACA CTTT										1680

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Thr	Lys	Ser	Asn	Gly	Glu	Glu	Pro	Lys	Met	Gly	Gly	Arg	Met	Glu
1				5					10					15	
Arg	Phe	Gln	Gln	Gly	Val	Arg	Lys	Arg	Thr	Leu	Leu	Ala	Lys	Lys	Lys
			20					25					30		
Val	Gln	Asn	Ile	Thr	Lys	Glu	Val	Val	Lys	Ser	Tyr	Leu	Phe	Arg	Asn
		35					40					45			

Ala	Phe	Val	Leu	Leu	Thr	Val	Thr	Ala	Val	Ile	Val	Gly	Thr	Ile	Leu
	50					55					60				
Gly	Phe	Thr	Leu	Arg	Pro	Tyr	Arg	Met	Ser	Tyr	Arg	Glu	Val	Lys	Tyr
65					70					75					80
Phe	Ser	Phe	Pro	Gly	Glu	Leu	Leu	Met	Arg	Met	Leu	Gln	Met	Leu	Val
				85					90					95	
Leu	Pro	Leu	Ile	Ile	Ser	Ser	Leu	Val	Thr	Gly	Met	Ala	Ala	Leu	Asp
			100					105						110	
Ser	Lys	Ala	Ser	Gly	Lys	Trp	Glu	Cys	Gly	Ala	Val	Val	Tyr	Tyr	Met
		115					120					125			
Thr	Thr	Thr	Ile	Ile	Ala	Val	Val	Ile	Gly	Ile	Ile	Ile	Val	Ile	Ile
	130					135					140				
Ile	His	Pro	Gly	Lys	Gly	Thr	Lys	Glu	Asn	Met	His	Arg	Glu	Gly	Lys
145					150					155					160
Ile	Val	Arg	Val	Thr	Ala	Ala	Asp	Ala	Phe	Leu	Asp	Leu	Ile	Arg	Asn
				165					170					175	
Met	Leu	Asn	Pro	Asn	Leu	Val	Glu	Ala	Cys	Phe	Lys	Gln	Phe	Lys	Thr
			180					185					190		
Asn	Tyr	Glu	Lys	Arg	Ser	Phe	Lys	Val	Pro	Ile	Gln	Ala	Asn	Glu	Thr
		195					200					205			
Leu	Val	Gly	Ala	Val	Ile	Asn	Asn	Val	Ser	Glu	Ala	Met	Glu	Thr	Leu
	210					215					220				
Thr	Arg	Ile	Thr	Glu	Glu	Leu	Val	Pro	Val	Pro	Gly	Ser	Val	Asn	Gly
225					230					235					240
Val	Asn	Ala	Leu	Gly	Leu	Val	Val	Phe	Ser	Met	Cys	Phe	Gly	Phe	Val
				245					250					255	
Ile	Gly	Asn	Met	Lys	Glu	Gln	Gly	Gln	Ala	Leu	Arg	Glu	Phe	Phe	Asp
			260					265					270		
Ser	Leu	Asn	Glu	Ala	Ile	Met	Arg	Leu	Val	Ala	Val	Ile	Met	Trp	Tyr
		275					280					285			
Ala	Pro	Val	Gly	Ile	Leu	Phe	Leu	Ile	Ala	Gly	Lys	Ile	Val	Glu	Met
	290					295					300				
Glu	Asp	Met	Gly	Val	Ile	Gly	Gly	Gln	Leu	Ala	Met	Tyr	Thr	Val	Thr
305					310					315					320

Val Ile Val Gly Leu Leu Ile His Ala Val Ile Val Leu Pro Leu Leu
325 330 335

Tyr Phe Leu Val Thr Arg Lys Asn Pro Trp Val Phe Ile Gly Gly Leu
340 345 350

Leu Gln Ala Leu Ile Thr Ala Leu Gly Thr Ser Ser Ser Ser Ala Thr
355 360 365

Leu Pro Ile Thr Phe Lys Cys Leu Glu Glu Asn Asn Gly Val Asp Lys
370 375 380

Arg Val Thr Arg Phe Val Leu Pro Val Gly Ala Thr Ile Asn Met Asp
385 390 395 400

Gly Thr Ala Leu Tyr Glu Ala Leu Ala Ala Ile Phe Ile Ala Gln Val
405 410 415

Asn Asn Phe Glu Leu Asn Phe Gly Gln Ile Ile Thr Ile Ser Ile Thr
420 425 430

Ala Thr Ala Ala Ser Ile Gly Ala Ala Gly Ile Pro Gln Ala Gly Leu
435 440 445

Val Thr Met Val Ile Val Leu Thr Ser Val Gly Leu Pro Thr Asp Asp
450 455 460

Ile Thr Leu Ile Ile Ala Val Asp Trp Phe Leu Asp Arg Leu Arg Thr
465 470 475 480

Thr Thr Asn Val Leu Gly Asp Ser Leu Gly Ala Gly Ile Val Glu His
485 490 495

Leu Ser Arg His Glu Leu Lys Asn Arg Asp Val Glu Met Gly Asn Ser
500 505 510

Val Ile Glu Glu Asn Glu Met Lys Lys Pro Tyr Gln Leu Ile Ala Gln
515 520 525

Asp Asn Glu Thr Glu Lys Pro Ile Asp Ser Glu Thr Lys Met
530 535 540

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1800 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: 5'UTR

(B) LOCATION: 1..33

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 34..1755

(ix) FEATURE:

(A) NAME/KEY: 3'UTR

(B) LOCATION: 1756..1800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATAGTGCTG AAGAGGAGGG GCGTTCCCAG ACC ATG GCA TCT ACG GAA GGT GCC	54
Met Ala Ser Thr Glu Gly Ala	
1 5	
AAC AAT ATG CCC AAG CAG GTG GAA GTG CGA ATG CCA GAC AGT CAT CTT	102
Asn Asn Met Pro Lys Gln Val Glu Val Arg Met Pro Asp Ser His Leu	
10 15 20	
GGC TCA GAG GAA CCC AAG CAC CGG CAC CTG GGC CTG CGC CTG TGT GAC	150
Gly Ser Glu Glu Pro Lys His Arg His Leu Gly Leu Arg Leu Cys Asp	
25 30 35	
AAG CTG GGG AAG AAT CTG CTG CTC ACC CTG ACG GTG TTT GGT GTC ATC	198
Lys Leu Gly Lys Asn Leu Leu Leu Thr Leu Thr Val Phe Gly Val Ile	
40 45 50 55	
CTG GGA GCA GTG TGT GGA GGG CTT CTT CGC TTG GCA TCT CCC ATC CAC	246
Leu Gly Ala Val Cys Gly Gly Leu Leu Arg Leu Ala Ser Pro Ile His	
60 65 70	
CCT GAT GTG GTT ATG TTA ATA GCC TTC CCA GGG GAT ATA CTC ATG AGG	294
Pro Asp Val Val Met Leu Ile Ala Phe Pro Gly Asp Ile Leu Met Arg	
75 80 85	
ATG CTA AAA ATG CTC ATT CTG GGT CTA ATC ATC TCC AGC TTA ATC ACA	342
Met Leu Lys Met Leu Ile Leu Gly Leu Ile Ile Ser Ser Leu Ile Thr	
90 95 100	
GGG TTG TCA GGC CTG GAT GCT AAG GCT AGT GGC CGC TTG GGC ACG AGA	390
Gly Leu Ser Gly Leu Asp Ala Lys Ala Ser Gly Arg Leu Gly Thr Arg	
105 110 115	
GCC ATG GTG TAT TAC ATG TCC ACG ACC ATC ATT GCT GCA GTA CTG GGG	438
Ala Met Val Tyr Tyr Met Ser Thr Thr Ile Ile Ala Ala Val Leu Gly	
120 125 130 135	

GTC ATT CTG GTC TTG GCT ATC CAT CCA GGC AAT CCC AAG CTC AAG AAG	486
Val Ile Leu Val Leu Ala Ile His Pro Gly Asn Pro Lys Leu Lys Lys	
140 145 150	
CAG CTG GGG CCT GGG AAG AAG AAT GAT GAA GTG TCC AGC CTG GAT GCC	534
Gln Leu Gly Pro Gly Lys Lys Asn Asp Glu Val Ser Ser Leu Asp Ala	
155 160 165	
TTC CTG GAC CTT ATT CGA AAT CTC TTC CCT GAA AAC CTT GTC CAA GCC	582
Phe Leu Asp Leu Ile Arg Asn Leu Phe Pro Glu Asn Leu Val Gln Ala	
170 175 180	
TGC TTT CAA CAG ATT CAA ACA GTG ACG AAG AAA GTC CTG GTT GCA CCA	630
Cys Phe Gln Gln Ile Gln Thr Val Thr Lys Lys Val Leu Val Ala Pro	
185 190 195	
CCG CCA GAC GAG GAG GCC AAC GCA ACC AGC GCT GAA GTC TCT CTG TTG	678
Pro Pro Asp Glu Glu Ala Asn Ala Thr Ser Ala Glu Val Ser Leu Leu	
200 205 210 215	
AAC GAG ACT GTG ACT GAG GTG CCG GAG GAG ACT AAG ATG GTT ATC AAG	726
Asn Glu Thr Val Thr Glu Val Pro Glu Glu Thr Lys Met Val Ile Lys	
220 225 230	
AAG GGC CTG GAG TTC AAG GAT GGG ATG AAC GTC TTA GGT CTG ATA GGG	774
Lys Gly Leu Glu Phe Lys Asp Gly Met Asn Val Leu Gly Leu Ile Gly	
235 240 245	
TTT TTC ATT GCT TTT GGC ATC GCT ATG GGG AAG ATG GGA GAT CAG GCC	822
Phe Phe Ile Ala Phe Gly Ile Ala Met Gly Lys Met Gly Asp Gln Ala	
250 255 260	
AAG CTG ATG GTG GAT TTC TTC AAC ATT TTG AAT GAG ATT GTA ATG AAG	870
Lys Leu Met Val Asp Phe Phe Asn Ile Leu Asn Glu Ile Val Met Lys	
265 270 275	
TTA GTG ATC ATG ATC ATG TGG TAC TCT CCC CTG GGT ATC GCC TGC CTG	918
Leu Val Ile Met Ile Met Trp Tyr Ser Pro Leu Gly Ile Ala Cys Leu	
280 285 290 295	
ATC TGT GGA AAG ATC ATT GCA ATC AAG GAC TTA GAA GTG GTT GCT AGG	966
Ile Cys Gly Lys Ile Ile Ala Ile Lys Asp Leu Glu Val Val Ala Arg	
300 305 310	
CAA CTG GGG ATG TAC ATG GTA ACA GTG ATC ATA GGC CTC ATC ATC CAC	1014
Gln Leu Gly Met Tyr Met Val Thr Val Ile Ile Gly Leu Ile Ile His	
315 320 325	
GGG GGC ATC TTT CTC CCC TTG ATT TAC TTT GTA GTG ACC AGG AAA AAC	1062
Gly Gly Ile Phe Leu Pro Leu Ile Tyr Phe Val Val Thr Arg Lys Asn	
330 335 340	

CCC TTC TCC CTT TTT GCT GGC ATT TTC CAA GCT TGG ATC ACT GCC CTG Pro Phe Ser Leu Phe Ala Gly Ile Phe Gln Ala Trp Ile Thr Ala Leu 345 350 355	1110
GGC ACC GCT TCC AGT GCT GGA ACT TTG CCT GTC ACC TTT CGT TGC CTG Gly Thr Ala Ser Ser Ala Gly Thr Leu Pro Val Thr Phe Arg Cys Leu 360 365 370 375	1158
GAA GAA AAT CTG GGG ATT GAT AAG CGT GTG ACT AGA TTC GTC CTT CCT Glu Glu Asn Leu Gly Ile Asp Lys Arg Val Thr Arg Phe Val Leu Pro 380 385 390	1206
GTT GGA GCA ACC ATT AAC ATG GAT GGT ACA GCC CTT TAT GAA GCG GTG Val Gly Ala Thr Ile Asn Met Asp Gly Thr Ala Leu Tyr Glu Ala Val 395 400 405	1254
GCC GCC ATC TTT ATA GCC CAA ATG AAT GGT GTT GTC CTG GAT GGA GGA Ala Ala Ile Phe Ile Ala Gln Met Asn Gly Val Val Leu Asp Gly Gly 410 415 420	1302
CAG ATT GTG ACT GTA AGC CTC ACA GCC ACC CTG GCA AGC GTC GGC GCG Gln Ile Val Thr Val Ser Leu Thr Ala Thr Leu Ala Ser Val Gly Ala 425 430 435	1350
GCC AGT ATC CCC AGT GCC GGG CTG GTC ACC ATG CTC CTC ATT CTG ACA Ala Ser Ile Pro Ser Ala Gly Leu Val Thr Met Leu Leu Ile Leu Thr 440 445 450 455	1398
GCC GTG GGC CTG CCA ACA GAG GAC ATC AGC TTG CTG GTG GCT GTG GAC Ala Val Gly Leu Pro Thr Glu Asp Ile Ser Leu Leu Val Ala Val Asp 460 465 470	1446
TGG CTG CTG GAC AGG ATG AGA ACT TCA GTC AAT GTT GTG GGT GAC TCT Trp Leu Leu Asp Arg Met Arg Thr Ser Val Asn Val Val Gly Asp Ser 475 480 485	1494
TTT GGG GCT GGG ATA GTC TAT CAC CTC TCC AAG TCT GAG CTG GAT ACC Phe Gly Ala Gly Ile Val Tyr His Leu Ser Lys Ser Glu Leu Asp Thr 490 495 500	1542
ATT GAC TCC CAG CAT CGA GTG CAT GAA GAT ATT GAA ATG ACC AAG ACT Ile Asp Ser Gln His Arg Val His Glu Asp Ile Glu Met Thr Lys Thr 505 510 515	1590
CAA TCC ATT TAT GAT GAC ATG AAG AAC CAC AGG GAA AGC AAC TCT AAT Gln Ser Ile Tyr Asp Asp Met Lys Asn His Arg Glu Ser Asn Ser Asn 520 525 530 535	1638
CAA TGT GTC TAT GCT GCA CAC AAC TCT GTC ATA GTA GAT GAA TGC AAG Gln Cys Val Tyr Ala Ala His Asn Ser Val Ile Val Asp Glu Cys Lys 540 545 550	1686

Glu	Val	Ser	Ser	Leu	Asp	Ala	Phe	Leu	Asp	Leu	Ile	Arg	Asn	Leu	Phe	165	170	175
Pro	Glu	Asn	Leu	Val	Gln	Ala	Cys	Phe	Gln	Gln	Ile	Gln	Thr	Val	Thr	180	185	190
Lys	Lys	Val	Leu	Val	Ala	Pro	Pro	Pro	Asp	Glu	Glu	Ala	Asn	Ala	Thr	195	200	205
Ser	Ala	Glu	Val	Ser	Leu	Leu	Asn	Glu	Thr	Val	Thr	Glu	Val	Pro	Glu	210	215	220
Glu	Thr	Lys	Met	Val	Ile	Lys	Lys	Gly	Leu	Glu	Phe	Lys	Asp	Gly	Met	225	230	235
Asn	Val	Leu	Gly	Leu	Ile	Gly	Phe	Phe	Ile	Ala	Phe	Gly	Ile	Ala	Met	245	250	255
Gly	Lys	Met	Gly	Asp	Gln	Ala	Lys	Leu	Met	Val	Asp	Phe	Phe	Asn	Ile	260	265	270
Leu	Asn	Glu	Ile	Val	Met	Lys	Leu	Val	Ile	Met	Ile	Met	Trp	Tyr	Ser	275	280	285
Pro	Leu	Gly	Ile	Ala	Cys	Leu	Ile	Cys	Gly	Lys	Ile	Ile	Ala	Ile	Lys	290	295	300
Asp	Leu	Glu	Val	Val	Ala	Arg	Gln	Leu	Gly	Met	Tyr	Met	Val	Thr	Val	305	310	315
Ile	Ile	Gly	Leu	Ile	Ile	His	Gly	Gly	Ile	Phe	Leu	Pro	Leu	Ile	Tyr	325	330	335
Phe	Val	Val	Thr	Arg	Lys	Asn	Pro	Phe	Ser	Leu	Phe	Ala	Gly	Ile	Phe	340	345	350
Gln	Ala	Trp	Ile	Thr	Ala	Leu	Gly	Thr	Ala	Ser	Ser	Ala	Gly	Thr	Leu	355	360	365
Pro	Val	Thr	Phe	Arg	Cys	Leu	Glu	Glu	Asn	Leu	Gly	Ile	Asp	Lys	Arg	370	375	380
Val	Thr	Arg	Phe	Val	Leu	Pro	Val	Gly	Ala	Thr	Ile	Asn	Met	Asp	Gly	385	390	395
Thr	Ala	Leu	Tyr	Glu	Ala	Val	Ala	Ala	Ile	Phe	Ile	Ala	Gln	Met	Asn	405	410	415
Gly	Val	Val	Leu	Asp	Gly	Gly	Gln	Ile	Val	Thr	Val	Ser	Leu	Thr	Ala	420	425	430

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Thr Leu Ala Ser Val Gly Ala Ala Ser Ile Pro Ser Ala Gly Leu Val
435 440 445

Thr Met Leu Leu Ile Leu Thr Ala Val Gly Leu Pro Thr Glu Asp Ile
450 455 460

Ser Leu Leu Val Ala Val Asp Trp Leu Leu Asp Arg Met Arg Thr Ser
465 470 475 480

Val Asn Val Val Gly Asp Ser Phe Gly Ala Gly Ile Val Tyr His Leu
485 490 495

Ser Lys Ser Glu Leu Asp Thr Ile Asp Ser Gln His Arg Val His Glu
500 505 510

Asp Ile Glu Met Thr Lys Thr Gln Ser Ile Tyr Asp Asp Met Lys Asn
515 520 525

His Arg Glu Ser Asn Ser Asn Gln Cys Val Tyr Ala Ala His Asn Ser
530 535 540

Val Ile Val Asp Glu Cys Lys Val Thr Leu Ala Ala Asn Gly Lys Ser
545 550 555 560

Ala Asp Cys Ser Val Glu Glu Glu Pro Trp Lys Arg Glu Lys
565 570

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR
- (B) LOCATION: 1..15

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 16..1590

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
- (B) LOCATION: 1591..1674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

57

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- 52 -

ATAGCGGCGA CAGCC ATG GGG AAA CCG GCG AGG AAA GGA TGC CCG AGT TGG	51
Met Gly Lys Pro Ala Arg Lys Gly Cys Pro Ser Trp	
1 5 10	
AAG CGC TTC CTG AAG AAT AAC TGG GTG TTG CTG TCC ACC GTG GCC GCG	99
Lys Arg Phe Leu Lys Asn Asn Trp Val Leu Leu Ser Thr Val Ala Ala	
15 20 25	
GTG GTG CTA GGC ATT ACC ACA GGA GTC TTG GTT CGA GAA CAC AGC AAC	147
Val Val Leu Gly Ile Thr Thr Gly Val Leu Val Arg Glu His Ser Asn	
30 35 40	
CTC TCA ACT CTA GAG AAA TTC TAC TTT GCT TTT CCT GGA GAA ATT CTA	195
Leu Ser Thr Leu Glu Lys Phe Tyr Phe Ala Phe Pro Gly Glu Ile Leu	
45 50 55 60	
ATG CGG ATG CTG AAA CTC ATC ATT TTG CCA TTA ATT ATA TCC AGC ATG	243
Met Arg Met Leu Lys Leu Ile Ile Leu Pro Leu Ile Ile Ser Ser Met	
65 70 75	
ATT ACA GGT GTT GCT GCA CTG GAT TCC AAC GTA TCC GGA AAA ATT GGT	291
Ile Thr Gly Val Ala Ala Leu Asp Ser Asn Val Ser Gly Lys Ile Gly	
80 85 90	
CTG CGC GCT GTC GTG TAT TAT TTC TGT ACC ACT CTC ATT GCT GTT ATT	339
Leu Arg Ala Val Val Tyr Tyr Phe Cys Thr Thr Leu Ile Ala Val Ile	
95 100 105	
CTA GGT ATT GTG CTG GTG GTG AGC ATC AAG CCT GGT GTC ACC CAG AAA	387
Leu Gly Ile Val Leu Val Val Ser Ile Lys Pro Gly Val Thr Gln Lys	
110 115 120	
GTG GGT GAA ATT GCG AGG ACA GGC AGC ACC CCT GAA GTC AGT ACG GTG	435
Val Gly Glu Ile Ala Arg Thr Gly Ser Thr Pro Glu Val Ser Thr Val	
125 130 135 140	
GAT GCC ATG TTA GAT CTC ATC AGG AAT ATG TTC CCT GAG AAT CTT GTC	483
Asp Ala Met Leu Asp Leu Ile Arg Asn Met Phe Pro Glu Asn Leu Val	
145 150 155	
CAG GCC TGT TTT CAG CAG TAC AAA ACT AAG CGT GAA GAA GTG AAG CCT	531
Gln Ala Cys Phe Gln Gln Tyr Lys Thr Lys Arg Glu Glu Val Lys Pro	
160 165 170	
CCC AGC GAT CCA GAG ATG AAC ATG ACA GAA GAG TCC TTC ACA GCT GTC	579
Pro Ser Asp Pro Glu Met Asn Met Thr Glu Glu Ser Phe Thr Ala Val	
175 180 185	
ATG ACA ACT GCA ATT TCC AAG AAC AAA ACA AAG GAA TAC AAA ATT GTT	627
Met Thr Thr Ala Ile Ser Lys Asn Lys Thr Lys Glu Tyr Lys Ile Val	
190 195 200	

52

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GGC ATG TAT TCA GAT	GGC ATA AAC GTC CTG	GGC TTG ATT GTC TTT TGC	675
Gly Met Tyr Ser Asp	Gly Ile Asn Val Leu	Gly Leu Ile Val Phe Cys	
205	210	215 220	
CTT GTC TTT GGA CTT GTC ATT GGA AAA ATG GGA GAA AAG GGA CAA ATT			723
Leu Val Phe Gly Leu Val Ile Gly Lys Met Gly Glu Lys Gly Gln Ile			
225	230	235	
CTG GTG GAT TTC TTC AAT GCT TTG AGT GAT GCA ACC ATG AAA ATC GTT			771
Leu Val Asp Phe Phe Asn Ala Leu Ser Asp Ala Thr Met Lys Ile Val			
240	245	250	
CAG ATC ATC ATG TGT TAT ATG CCA CTA GGT ATT TTG TTC CTG ATT GCT			819
Gln Ile Ile Met Cys Tyr Met Pro Leu Gly Ile Leu Phe Leu Ile Ala			
255	260	265	
GGG AAG ATC ATA GAA GTT GAA GAC TGG GAA ATA TTC CGC AAG CTG GGC			867
Gly Lys Ile Ile Glu Val Glu Asp Trp Glu Ile Phe Arg Lys Leu Gly			
270	275	280	
CTT TAC ATG GCC ACA GTC CTG ACT GGG CTT GCA ATC CAC TCC ATT GTA			915
Leu Tyr Met Ala Thr Val Leu Thr Gly Leu Ala Ile His Ser Ile Val			
285	290	295 300	
ATT CTC CCG CTG ATA TAT TTC ATA GTC GTA CGA AAG AAC CCT TTC CGA			963
Ile Leu Pro Leu Ile Tyr Phe Ile Val Val Arg Lys Asn Pro Phe Arg			
305	310	315	
TTT GCC ATG GGA ATG GCC CAG GCT CTC CTG ACA GCT CTC ATG ATC TCT			1011
Phe Ala Met Gly Met Ala Gln Ala Leu Leu Thr Ala Leu Met Ile Ser			
320	325	330	
TCC AGT TCA GCA ACA CTG CCT GTC ACC TTC CGC TGT GCT GAA GAA AAT			1059
Ser Ser Ser Ala Thr Leu Pro Val Thr Phe Arg Cys Ala Glu Glu Asn			
335	340	345	
AAC CAG GTG GAC AAG AGG ATC ACT CGA TTC GTG TTA CCC GTT GGT GCA			1107
Asn Gln Val Asp Lys Arg Ile Thr Arg Phe Val Leu Pro Val Gly Ala			
350	355	360	
ACA ATC AAC ATG GAT GGG ACC GCG CTC TAT GAA GCA GTG GCA GCG GTG			1155
Thr Ile Asn Met Asp Gly Thr Ala Leu Tyr Glu Ala Val Ala Ala Val			
365	370	375 380	
TTT ATT GCA CAG TTG AAT GAC CTG GAC TTG GGC ATT GGG CAG ATC ATC			1203
Phe Ile Ala Gln Leu Asn Asp Leu Asp Leu Gly Ile Gly Gln Ile Ile			
385	390	395	
ACC ATC AGT ATC ACG GCC ACA TCT GCC AGC ATC GGA GCT GCT GGC GTG			1251
Thr Ile Ser Ile Thr Ala Thr Ser Ala Ser Ile Gly Ala Ala Gly Val			
400	405	410	

53

CCC Pro	CAG Gln	GCT Ala	GGC Gly	CTG Leu	GTG Val	ACC Thr	ATG Met	GTG Val	ATT Ile	GTG Val	CTG Leu	AGT Ser	GCC Ala	GTG Val	GGC Gly	1299
		415				420						425				
CTG Leu	CCC Pro	GCC Ala	GAG Glu	GAT Asp	GTC Val	ACC Thr	CTG Leu	ATC Ile	ATT Ile	GCT Ala	GTC Val	GAC Asp	TGG Trp	CTC Leu	CTG Leu	1347
		430				435				440						
GAC Asp 445	CGG Arg	TTC Phe	AGG Arg	ACC Thr	ATG Met	GTC Val	AAC Asn	GTC Val	CTT Leu	GGT Gly	GAT Asp	GCT Ala	TTT Phe	GGG Gly	ACG Thr 460	1395
				450						455						
GGC Gly	ATT Ile	GTG Val	GAA Glu	AAG Lys	CTC Leu	TCC Ser	AAG Lys	AAG Lys	GAG Glu	CTG Leu	GAG Glu	CAG Gln	ATG Met	GAT Asp	GTT Val	1443
				465				470						475		
TCA Ser	TCT Ser	GAA Glu	GTC Val	AAC Asn	ATT Ile	GTG Val	AAT Asn	CCC Pro	TTT Phe	GCC Ala	TTG Leu	GAA Glu	TCC Ser	ACA Thr	ATC Ile	1491
		480						485				490				
CTT Leu	GAC Asp	AAC Asn	GAA Glu	GAC Asp	TCA Ser	GAC Asp	ACC Thr	AAG Lys	AAG Lys	TCT Ser	TAT Tyr	GTC Val	AAT Asn	GGA Gly	GGC Gly	1539
		495				500						505				
TTT Phe	GCA Ala	GTA Val	GAC Asp	AAG Lys	TCT Ser	GAC Asp	ACC Thr	ATC Ile	TCA Ser	TTC Phe	ACC Thr	CAG Gln	ACC Thr	TCA Ser	CAG Gln	1587
		510				515				520						
TTC Phe 525	TAGGGCCCCT		GGCTGCAGAT		GACTGGAAAC		AAGGAAGGAC		ATTTCGTGAG							1640
AGTCATCTCA AACACGGCTT AAGGAAAAGA GAAA																1674

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Lys Pro Ala Arg Lys Gly Cys Pro Ser Trp Lys Arg Phe Leu
1 5 10 15

Lys Asn Asn Trp Val Leu Leu Ser Thr Val Ala Ala Val Val Leu Gly
20 25 30

54
-35-

Ile Thr Thr Gly Val Leu Val Arg Glu His Ser Asn Leu Ser Thr Leu
35 40 45

Glu Lys Phe Tyr Phe Ala Phe Pro Gly Glu Ile Leu Met Arg Met Leu
50 55 60

Lys Leu Ile Ile Leu Pro Leu Ile Ile Ser Ser Met Ile Thr Gly Val
65 70 75 80

Ala Ala Leu Asp Ser Asn Val Ser Gly Lys Ile Gly Leu Arg Ala Val
85 90 95

Val Tyr Tyr Phe Cys Thr Thr Leu Ile Ala Val Ile Leu Gly Ile Val
100 105 110

Leu Val Val Ser Ile Lys Pro Gly Val Thr Gln Lys Val Gly Glu Ile
115 120 125

Ala Arg Thr Gly Ser Thr Pro Glu Val Ser Thr Val Asp Ala Met Leu
130 135 140

Asp Leu Ile Arg Asn Met Phe Pro Glu Asn Leu Val Gln Ala Cys Phe
145 150 155 160

Gln Gln Tyr Lys Thr Lys Arg Glu Glu Val Lys Pro Pro Ser Asp Pro
165 170 175

Glu Met Asn Met Thr Glu Glu Ser Phe Thr Ala Val Met Thr Thr Ala
180 185 190

Ile Ser Lys Asn Lys Thr Lys Glu Tyr Lys Ile Val Gly Met Tyr Ser
195 200 205

Asp Gly Ile Asn Val Leu Gly Leu Ile Val Phe Cys Leu Val Phe Gly
210 215 220

Leu Val Ile Gly Lys Met Gly Glu Lys Gly Gln Ile Leu Val Asp Phe
225 230 235 240

Phe Asn Ala Leu Ser Asp Ala Thr Met Lys Ile Val Gln Ile Ile Met
245 250 255

Cys Tyr Met Pro Leu Gly Ile Leu Phe Leu Ile Ala Gly Lys Ile Ile
260 265 270

Glu Val Glu Asp Trp Glu Ile Phe Arg Lys Leu Gly Leu Tyr Met Ala
275 280 285

Thr Val Leu Thr Gly Leu Ala Ile His Ser Ile Val Ile Leu Pro Leu
290 295 300

55

55
-36-

Ile Tyr Phe Ile Val Val Arg Lys Asn Pro Phe Arg Phe Ala Met Gly
305 310 315 320

Met Ala Gln Ala Leu Leu Thr Ala Leu Met Ile Ser Ser Ser Ser Ala
325 330 335

Thr Leu Pro Val Thr Phe Arg Cys Ala Glu Glu Asn Asn Gln Val Asp
340 345 350

Lys Arg Ile Thr Arg Phe Val Leu Pro Val Gly Ala Thr Ile Asn Met
355 360 365

Asp Gly Thr Ala Leu Tyr Glu Ala Val Ala Ala Val Phe Ile Ala Gln
370 375 380

Leu Asn Asp Leu Asp Leu Gly Ile Gly Gln Ile Ile Thr Ile Ser Ile
385 390 395 400

Thr Ala Thr Ser Ala Ser Ile Gly Ala Ala Gly Val Pro Gln Ala Gly
405 410 415

Leu Val Thr Met Val Ile Val Leu Ser Ala Val Gly Leu Pro Ala Glu
420 425 430

Asp Val Thr Leu Ile Ile Ala Val Asp Trp Leu Leu Asp Arg Phe Arg
435 440 445

Thr Met Val Asn Val Leu Gly Asp Ala Phe Gly Thr Gly Ile Val Glu
450 455 460

Lys Leu Ser Lys Lys Glu Leu Glu Gln Met Asp Val Ser Ser Glu Val
465 470 475 480

Asn Ile Val Asn Pro Phe Ala Leu Glu Ser Thr Ile Leu Asp Asn Glu
485 490 495

Asp Ser Asp Thr Lys Lys Ser Tyr Val Asn Gly Gly Phe Ala Val Asp
500 505 510

Lys Ser Asp Thr Ile Ser Phe Thr Gln Thr Ser Gln Phe
515 520 525

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

56

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-57-

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGGTACC GCCATGGAGA AGAGCAAC

28

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGCGTCTAGA TCACAGAACC GACTCCTTG

29

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGGTACC AATATGACTA AAAGCAATG

29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGCGTCTAGA CTACATCTTG GTTCACTG

29

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs

57

57
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- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGGGTACC ACCATGGCAT CTACGGAAG

29

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCGTCTAGA TTATTTCTCA CGTTTCCAAG

30

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCGGGTACC GCCATGGGGA AACCGGCG

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCGGGATCC CTAGAACTGT GAGGTCTG

28

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